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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file Seq140-aay87247.res made by tport on Wed 14 Jan 104 14:59:51-PST.

Query sequence being compared: US-10-006-485A-140 (1-311)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-10-006-485A-140 (1-311) with:
File: aay87247.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
E 5-
J -
I -
N -
Y -
Z -
3
2
1
0

SCORE 0 34 69 103 138 172 207 241 276 310
STDDEV

PARAMETERS

Similarity matrix PAM-150 K-tuple 1
Threshold level of sim. 16%
Mismatch penalty 1 Joining penalty 20
Gap penalty 5.00 Window size 311
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 310 Median 0 Standard Deviation 0.00

Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00

Number of residues: 311
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name Description Length Score Score Init. Opt. Sig. Frame

1. aay87247 Human signal peptide contain 311 310 310 0.00 0

1. US-10-006-485A-140 (1-311).
aay87247 Human signal peptide containing protein HSP-24 SE

Initial Score = 310 Optimized Score = 310 Significance = 0.00
Residue Identity = 99% Matches = 309 Mismatches = 1
Gaps = 0 Conservative Substitutions = 1

X 10 20 30 40 50 60 70
MGVPTALEAGSWKGSILFPLFLAASLGVAFAKVAATPYSLVCPGQVNTLTCLLGPVKGHDVTFYKTM
MGVPTALEAGSWKGSILFPLFLAASLGVAFAKVAATPYSLVCPGQVNTLTCLLGPVKGHDVTFYKTM
X 10 20 30 40 50 60 70

YRSSRGEVQTCSEFRRIIRNUTFDLHLHGHGHOANTSHDLAORHGLSASDHGHPSTMTNLTLLDSGLY
YRSSRGEVQTCSEFRRIIRNUTFDLHLHGHGHOANTSHDLAORHGLSASDHGHPSTMTNLTLLDSGLY
YRSSRGEVQTCSEFRRIIRNUTFDLHLHGHGHOANTSHDLAORHGLSASDHGHPSTMTNLTLLDSGLY
X 80 90 100 110 120 130 140

CCLVVEIRHHSHRHRYHGMELQVOTGKAPNSCVVYBSSQDSSENTITAAALATGACIVGILCLPLILLVY
CCLVVEIRHHSHRHRYHGMELQVOTGKAPNSCVVYBSSQDSSENTITAAALATGACIVGILCLPLILLVY
CCLVVEIRHHSHRHRYHGMELQVOTGKAPNSCVVYBSSQDSSENTITAAALATGACIVGILCLPLILLVY
X 150 160 170 180 190 200 210

KORQASNNRRRAOELVMDSDNIQIENPGFEASPPAGIPEAKVRHPLSYAQRQPSGGRHLSESTPLSP
KORQASNNRRRAOELVMDSDNIQIENPGFEASPPAGIPEAKVRHPLSYAQRQPSGGRHLSESTPLSP
KORQASNNRRRAOELVMDSDNIQIENPGFEASPPAGIPEAKVRHPLSYAQRQPSGGRHLSESTPLSP
X 220 230 240 250 260 270 280

PGPGDVFFPSLDVPPDSPNFEVI
PGPGDVFFPSLDVPPDSPNFEVI
PGPGDVFFPSLDVPPDSPNFEVI
X 290 300 310